

hmdr1	1	MDLEGRNGGAKKNF.....FKLNKSEKDKKEKPT..VSFSMFYRNWLDKLYMVVGTAAIITHGAGLPLMLVFGEMTDIFANAGNLEDLMSITNRSINDTGF
atpac	1	~~~~~MSETNTDAKTPAEAEKKKEQSLFFKLFSPADKFDYLLMFVGSLSGAIHVGSSMPVFFLLFCQMVNGGKQNMDEL.....s
consensus	1	md e g a l s dr kkk vgv lFryadw Dkl M lctlaaiHGs lPlmmivFgemtd fa
hmdr1	105	MN..LEEDMTRAYXXSGIGAGVLVAAAYIQVSWCLAAQRQIHKIRKQFFHAINRQEI GWFDVH.DVGELNTRLTDDVSKINEVIGDKIGMFFQSMATEFTFGIVGFTTRG
hmdr1	102	SNSSLEEEEMAIYAYYYTGIGAGVLIVAYIQVSLWCLAAQRQIHKIRKQFFHAINRQEI GWFDVH.DVGELNTRLTDDVSKINDIGDKIGMFFQSIITFLAGTIGFISG
atpac	77	..HQMVHEVSRYSLYFVYLGVLVVCFSYSAEIAQWMSYGERQVAAALRKRYLEAVLQDVDFDRTDARTGDIVSVSTDTLLVQDDAISEKVGNIHYLSFTFLAGLVVGVFSA
atpgp1	80	..EKMEEVLYKALYFLVVGAIIWASWAEISWMSYGERQVTKMRIKYLEAALNQDIQFDETEVTSDDVFAINTDAVMVQDAISEKLGNIHYMATFVSGFIVGFTAV
atpgp2	73	..KOASHRVAKYSLDFVYLSVAIFSSWLEVACWMTGERQAKMRRAYLRSLMSQDISLFDTEASTGEVISAITSIDLVDQDALSEKVGNIHYISRFIAGFAIGFTSV
consensus	111	k leemtrYayyyvglgagvly ayiqvs W laagRQirkir kfhailrQeigwFdi tgelntrltdDiskindgigKvGmfq vatFlagfivGfi g
hmdr3	214	WKLTLVIMAI SPILGLSAAVWAKILSAFSDKELAAAYAKAGAVAEALGAIRTVTAFGGQNKELERYQKHLENAKEIGIKKAI SANISMGIAFLIIYASALAFWYGSTLV
hmdr2	211	WKLTLVIMAI SPILGLSTAVWAKILSTFSDKELAAAYAKAGAVAEALGAIRTVTAFGGQNKELERYQKHLENAKIGIKKAI SANISMGIAFLIIYASALAFWYGSTLV
hmdr1	212	WKLTLVILAI SPVLGLSAAVWAKILSTFSDKELAAAYAKAGAVAEALGAIRTVTAFGGQNKELERYQKHLENAKIGIKKAI SANISMGIAFLIIYASALAFWYGSTLV
hmdr1	211	WKLTLVILAI SPVLGLSAAVWAKILSTFSDKELAAAYAKAGAVAEALGAIRTVTAFGGQNKELERYQKHLENAKIGIKKAI SANISMGIAFLIIYASALAFWYGSTLV
atpac	185	WKLALISVAVIPGIAFAGGLYAYTLTGITSKRSYANAGVIAEQAIQAQVTVYSYVGESKALNAYSDAIQYTLKLGKAGMAKGLGLGCTYGIACMSWALVFWYAGVFI
atpgp1	188	WQLALVTLAVPLI AVIGGIHTTTL SKLSQESLSQAGNIVEQTVVQIRVMAFVGESRASQAYSSALAKIAQKLGKYGKGLAGMGLGATYFVVFCCYALLWYGGYIV
atpgp2	181	WQISLVTLISIVPLIALAGGIYAFVAIGLIARVRKSYIKAGEIAEAEVIGNVRTVQAFTGEERAVRLREALENTYKYGKAGLTGKGLGSMHCVLFLSWALLVWFTSVVV
consensus	221	WkltlvilaisPiiglsaavwakils fs kel ayakAGavaEe lgairtViafgGq keleriyq le akkiGiKkaisa ismG afliiyasyAlafwygstlv
hmdr3	324	ISKEYTIGNAMTVFFSILIGAFSVGQAAPCIDAFANARGAAAVIFDIIDNNPKIDSFSERGHKPDSTIKGNLEFNVDVHFSYPSRANVKILKGLNLKVQSGQTVALVGS
hmdr2	321	ISKEYTIGNAMTVFFSILIGAFSVGQAAPCIDAFANARGAAAVIFDIIDNNPKIDSFSERGHKPDSTIKGNLEFNVDVHFSYPSRANVKILKGLNLKVQSGQTVALVGS
hmdr1	322	LSGEYSIGQVLT VFFSVLIGAFSVGQAAPSIDAFANARGAAVEIFKIIDNKPSIDSYSKSGHKPDNKGKLEFNVDVHFSYPSRANVKILKGLNLKVQSGQTVALVGS
hmdr1	321	LSNEYSIGEVLT VFFSVLIGAFSVGQAAPSIDAFANARGAAVEIFKIIDNEPSIDSYSKSGHKPDNKGKLEFNVDVHFSYPSRANVKILKGLNLKVQSGQTVALVGS
atpac	295	RNGQTDGGAFTAI FSAIVGMSLQGSFSLGAFSGKAAGYKIMEIINORPTIIQDPLDQKCLDQVHGNIEFKDVTFSYSPRPDVMIFRNFNIFFPFGKTAVVVGSGS
atpgp1	298	RHHLTGGLAIATMFVMI GGLALGQSAPMAAFKAKVAAAKIFRIIDHKPTIERNSESGVELDSTVGLVELKQWVDFSYSPRPDVKILNNFCLSVPGAKTIALVGS
atpgp2	291	HKDIADGGKSTTMLNVVIAGLSLQAAPDISAFVRAKAAAVPIFKMIERTVTTKTSKSGRKLGVGDGHIQFKDATFSYSPRPDVVIFDRNLAIIPAGKIVALVGS
consensus	331	is eytiG antvffsiligafsvGqaap idaFanaargAay ifkiidn psidsfs Ghkpd ikGnlefkdvHfSyPSR evkilkgnlnkv sgqtvalivG sGc

W_A

FIGURE 1

hmdr3 434 GKSTTVQLIQRLYDPDEGTINIDGQDIRNFNVNRYLREIIGVVSQEPVLFSTTIAENICYGRNVMTDEIKKAVKEANAYFIMKLPKQKFDFTLVGERGAQLSGGQKQRIAI
hmdr2 431 GKSTTVQLLQRLYDPTGKISIDGQDIRNFNVNRYLREIIGVVSQEPVLFSTTIAENICYGRNVMTDEIKKAVKEANAYFIMKLPKQKFDFTLVGERGAQLSGGQKQRIAI
hmdr1 432 GKSTTVQLMQRLYDPTGKISIDGQDIRNFNVNRYLREIIGVVSQEPVLFSTTIAENICYGRNVMTDEIKKAVKEANAYFIMKLPKQKFDFTLVGERGAQLSGGQKQRIAI
nmldr1 431 GKSTTVQLMQRLYDPTGKISIDGQDIRNFNVNRYLREIIGVVSQEPVLFSTTIAENICYGRNVMTDEIKKAVKEANAYFIMKLPKQKFDFTLVGERGAQLSGGQKQRIAI
atpac 405 GKSTTVSLIERFYDPNPGQILLDQVEIKTLQKFLRQIGLVNQEPALFATSIKENILYKQPDATVEEAAANAHAFITLLPKGYDTQVGERGLQSLSGGQKQRIAI
atpgp1 408 GKSTTVSLIERFYDPNPGQILLDQVEIKTLQKFLRQIGLVNQEPALFATSIKENILYKQPDATVEEAAANAHAFITLLPKGYDTQVGERGLQSLSGGQKQRIAI
atpgp2 401 GKSTTVSLIERFYDPNPGQILLDQVEIKTLQKFLRQIGLVNQEPALFATSIKENILYKQPDATVEEAAANAHAFITLLPKGYDTQVGERGLQSLSGGQKQRIAI
consensus 441 GKSTTVQLIQRLYDPTGKISIDGQDIRNFNVNRYLREIIGVVSQEPVLFSTTIAENICYGRNVMTDEIKKAVKEANAYFIMKLPKQKFDFTLVGERGAQLSGGQKQRIAI

hmdr3 544 ARALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......F.
hmdr2 541 ARALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......FE
hmdr1 542 ARALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......FE
nmldr1 541 ARALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......FE
atpac 515 ARALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......FE
atpgp1 518 ARALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......FE
atpgp2 511 SRALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......FE
consensus 551 ARALVRNPKILLDEATSDTESAEVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFEDGVIVEQSGHSELMKK..EGVYFKLVNMQTSQIQSE.......FE

hmdr3 643 .ELNDEKAATRMAPNGWKSRLFRHSTQKNLKNQMCQK...SLDVEDGLEANVPVFLKVLKLNKTEWPFVVGTVCAIANGGLOPAFVSIFSEIIAIFGPGDD.AVK
hmdr2 641 VELSDKAAGDVAPNGWKSRLFRHSTQKNLKNQMCQK...SLDVEDGLEANVPVFLKVLKLNKTEWPFVVGTVCAIANGGLOPAFVSIFSEIIAIFGPGDD.AVK
hmdr1 642 DESKSEIDALEMSNDSSRLIRKSTRSVRGSAQOE...RLDEETNEIDANVPVFLKVLKLNKTEWPFVVGTVCAIANGGLOPAFVSIFSEIIAIFGPGDD.AVK
nmldr1 641 YGSQSDTDASELTSSEESKPLIR.RSIYRSVHRKQOE...RLSMKEAEDVDVPLVSVFWRILNINLSEWPLYLVGVLCVINGCIPQVFAIVFSRIVGVFSRDDHETK
atpac 623 LSHLSLTKSLSL...RGSRLNLSYSYTGADGRIEMISNAETDRKTRA...PENYFRLKLNSEWPLYLVGVLCVINGCIPQVFAIVFSRIVGVFSRDDHETK
atpgp1 628 ARNSVSSPIMTRNSSYGRSPYRRLSDFTSDFSLSDASSYPNYRNEKLAFOOANSFWRILAKMNSPEWKYALIGSVGICSAFFAYVLSAVLSVYVYNNPDHEYMI
atpgp2 620 IKYS.....RELSTRSSFCSESR.ESVTRPDGADPSKKVKTVG...RLYSMIRPDMMYGVGCTICAFIAGSQMLFALGVSQAL.VSYYSGWDETO
consensus 661 s e a m ks l R s s qd r d d le vp vsfwrvlkln tewpy vvtvcaialng lqp failis iiafv dd vk

hmdr3 748 QOKCNIFSLIFLGLISFTFFLOGFTFGKAGEILTRRLRSMAFKAMLRQDMSWFDHDKNSTGALSTRLATDAAQVQATGTRLALIAQNIANLGTGIIISFIYGWQLT
hmdr2 745 QOKCNIFSLIFLGLISFTFFLOGFTFGKAGEILTRRLRSMAFKAMLRQDMSWFDHDKNSTGALSTRLATDAAQVQATGTRLALIAQNIANLGTGIIISFIYGWQLT
hmdr1 749 QOKCNIFSLIFLGLISFTFFLOGFTFGKAGEILTRRLRSMAFKAMLRQDMSWFDHDKNSTGALSTRLATDAAQVQATGTRLALIAQNIANLGTGIIISFIYGWQLT
nmldr1 747 QOKCNIFSLIFLGLISFTFFLOGFTFGKAGEILTRRLRSMAFKAMLRQDMSWFDHDKNSTGALSTRLATDAAQVQATGTRLALIAQNIANLGTGIIISFIYGWQLT
atpac 725 RK.TKEYVFIYIGAGLYAVGAYLIQHYFFSINGENLTVRRMMLSAIRNEVGEDEHNSLIAARLATDANNVSAIRSVLQNMVTSLLTSFTVAFIWEVRVS
atpgp1 738 QK.IDKCYLLIGLSSAALVENTLQHSFWDIVGENLTVRRMMLSAIRNEVGEDEHNSLIAARLATDANNVSAIRSVLQNMVTSLLTSFTVAFIWEVRVS
atpgp2 707 KE.IKKAILFCCASVITLIVTIBHCFTGMEGRLTVRRMMLSAIRNEVGEDEHNSLIAARLATDANNVSAIRSVLQNMVTSLLTSFTVAFIWEVRVS
consensus 771 rq nifsliflglisfitflgqftfgkageiltrvr mvfkamLRQDMSWFDHDKNSTGALSTRLATDAAQVQATGTRLALIAQNIANLGTGIIISFIYGWQLT

FIGURE 2

858 LLLAVVPITIAVSGIVEMKLIAGNAKRDKKELEAAGKIATEAIEINRTVVSILTQERKFESMYVEKLYGPRNSV..QKAHIXGITESISQAEMFVSAGCFRFGAYLIVN
855 LLLSVVPFIAGVIGEMKMLAGNAKRDKKEAAGKIATEAIEINRTVVSILTQERKFESMYVEKLGHPYNSV..RKAHIXGITESISQAEMFVSAGCFRFGSYLIVN
859 LLLAIVPIAIAGVVEMKMLSGQALKDKKELEGAGKIATEAIEINRTVVSILTQEQFEHMYAQSLQVPYNSL..RKAHIGITESTTQAMMFVSAGCFRFGAYLVAH
857 LLLVVIIPLIIVLGGIIEMLKLSGQALKDKKEISGKIATEAIEINRTVVSILTREQFEHMYAQSLQVPYNSL..RKAHIVGITESTTQAMMFVSAGCFRFGAYLVAQ
834 LLLIGTFPLLVLANFAQQLSLKGFAGDTAKAHAKTSMIAGEGVSINRTVAAFNAQKILSLFCHHELVPKRSLSIYRSQTSGLFGLSQALALYSEALINWYGAHLVSK
847 LILVAVFPVVAAATVLOQEMFTGSGDLEAAHAKGTQAGEAIAINRTVAAFNSEAKIVRLYXANLEPPIKR..CFWKGQIAGSGYGYAQFCLYASVALGYASWLVKH
816 LVVLIATYPIVISGHISEKLFMQGYGGDLNKAYLKANMLAGESVSNIRTVAAAFCAEEKILELYSRELLPEPSKSS..FRGQIAGLFGYGVSQFFIFSSYGLALWYGSTLMDK
consensus 881 LlllavvPlivvagivemkil Gna rdkk le agkIatEaIenrtvvsilt e kfesmy L Pynsv rkahiyGItfssisQa myfSyaGcfrfgaylv h

W_A

966 GHMFRDVLVFSaIVFGAVALGHASFPADYAKAKLSAAHLFMLFERQPLIDSYSSEGL.KPDKFEGNITFNEVVFNYPTRANVPVLQGLSLEVKKGQTILALVGSsGCG
963 GHMRFKDVILVFSaIVLGAVALGHASFPADYAKAKLSAAYLFSIFERQPLIDSYSSEGL.WPDKFEGSVTFNEVVFNYPTRANVPVLQGLSLEVKKGQTILALVGSsGCG
967 KLMSEFEDVLLVFSaVFGAMAVGQVSSFPADYAKAKLSAAHIIIMIEKTPLIDSYSSEGL.MENTLEGNVTFGEVFNYPTRANVPVLQGLSLEVKKGQTILALVGSsGCG
965 QLMTFENVMLVFSaVFGAMAAGNTSSFPADYAKAKVSASHIIRIEKTEPLIDSYSSEGL.KPTLLEGNVKNFNGVFNYPTRANVPVLQGLSLEVKKGQTILALVGSsGCG
944 GVSTFSKVIKVFVVLVITANSVAETVSLAPEIIRGGEAVGSVSVLDRQTRIDPDADADPV.ETIRGDIIEFRHVDFAYPSPRDPVDFNLRIRAGHSQALVGAAGSGG
955 GISDFSKTIRVFMVMSANGAETILTAPDFIKGGQAMRSVFELLDKRTIEPDDPTTPVDRLRGEVELKHIDFSYSPRPDIQIFRDLSLRAGAKTILALVGSsGCG
924 GLAGFKSVMTFMVLIVTALAMGETLALAPDLLKGNQWVASVFEILDRKTOIV...GETSEELNNVEGTIELKGVHFSYSPRPDVIFRDFDLIVRAGKSMALVGSsGCG
consensus 991 glm F vilvFsaivlgAvalg tssfAPdyakaklsaa lf Iier p Idsys egl pd leG v f v FnyPcRpdvpvliqglSlevkkGqtlALVGSsGCG

1075 KSTVVQLLERFYDPLAGTVLLDGOEAKKLNQWLRAQLGIVSQEPILFDCSIAENIAYGDNRSRVVSQDEIVSAAKAAIHPIETLPHKYETRVGDKGTOLSGGQKORIA
1072 KSTVVQLLERFYDPMAGSVLLDGOEAKKLNQWLRAQLGIVSQEPILFDCSIAENIAYGDNRSRVVPHDEIVRAAKEANIHPIETLPKYNTRVGDKGTOLSGGQKORIA
1076 KSTVVQLLERFYDPLAGKVLLDGGKETKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIA
1074 KSTVVQLLERFYDPMAGSVFLDGKEIKQLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNRSRAVSHEEIVRAAKEANIHOFIDSLPKYNTRVGDKGTOLSGGQKORIA
1053 KSSVIAMERFYDLLAGKVMIDGKDILRLNLKSLRLKTLGIVQEPALFAATI FDNIAYGKDG..ATESEVIDAARAANAAGHFI SGLPEGYKTPVGERGVOLSGGQKORIA
1065 KSSVISLIQRFYEPSSGRVMDGKDILRKNLKAIRKHIAIVQEPCLFGTTIYENIAYGHEC..ATEAEIIQAATLASAHKFISALPEGYKTPVGERGVOLSGGQKORIA
1031 KSSVISLILRFYDPTAGKVMIEGKDILKLDLKAIRKHILGIVQEPALFATTIYENIAYNEG..ASQSEVVESAMLANAHSFITSLPESYSTKVGERGVOLSGGQKORIA
consensus 1101 KstVvqlleRFYdplagkvllldgkeikklnvqwlRahlgivSQEPiLFdcslaeNiaYgdnsr vs dEiv aak AniH FietLPdky TrvcdkgtQlsgGQKORIA

FIGURE 3

W_B

hmdr3	1185	IARALIROPQILLLLDEATSEKVVQAEALDKAREGTCIVIAHRLSTIQNADLIWVFQNGRVKKEHGHQQLAQK..GIYFSMVSVOAGTONL~~~~~
mmdr2	1182	IARALIROPVLLLLDEATSEKVVQAEALDKAREGTCIVIAHRLSTIQNADLIWVFQNGRVKKEHGHQQLAQK..GIYFSMNIQAGTONL~~~~~
hmdr1	1186	IARALVROPHILLLLDEATSEKVVQAEALDKAREGTCIVIAHRLSTIQNADLIWVFQNGRVKKEHGHQQLAQK..GIYFSMVSVOAGTKRQ~~~~~
mmdr1	1184	IARALVROPHILLLLDEATSEKVVQAEALDKAREGTCIVIAHRLSTIQNADLIWVFQNGRVKKEHGHQQLAQK..GIYFSM..VQAGAKRS~~~~~
atpac	1161	IARAVLKNPTVLLLLDEATSEKVVQAEALDKAREGTCIVIAHRLSTIRGVDCIGVIOGGRIVEOGSHSELV.SRPEGAYSRLQLQTHRI*~~~~~
atpgp1	1173	IARALVRKAEIMLLDEATSEKVVQAEALDKAREGTCIVIAHRLSTIRNAHVIAVIDGKVAEQGSHSHLLKNHPDGIYARMIQLQRFTTQVIGMTSGSSSRVK
atpgp2	1139	IARAILKNPAILLLLDEATSEKVVQAEALDKAREGTCIVIAHRLSTIKNADTISVLHGGKIVEOGSHRKLVLNK.SGPYFKLISLQQQQQF~~~~~
consensus	1211	IARALirqp iLLlDEATSEKvvQeAlDkaregTciVIAHRLSTiqnadliWvi nckvkEhGtHqqLlaqk GiYfsmv vQagt
hmdr3	1280	~~~~~
mmdr2	1277	~~~~~
hmdr1	1281	~~~~~
mmdr1	1277	~~~~~
atpac	1255	~~~~~
atpgp1	1283	EDDA
atpgp2	1234	~~~~~
consensus	1321	

FIGURE 4

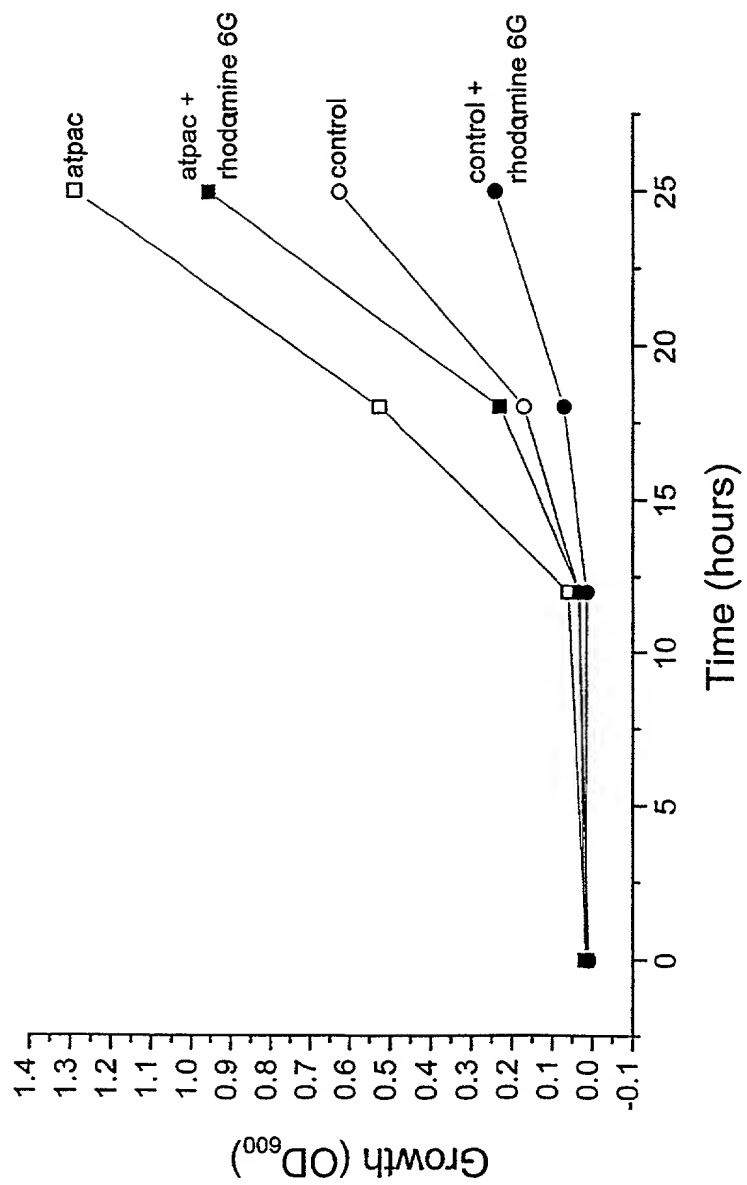
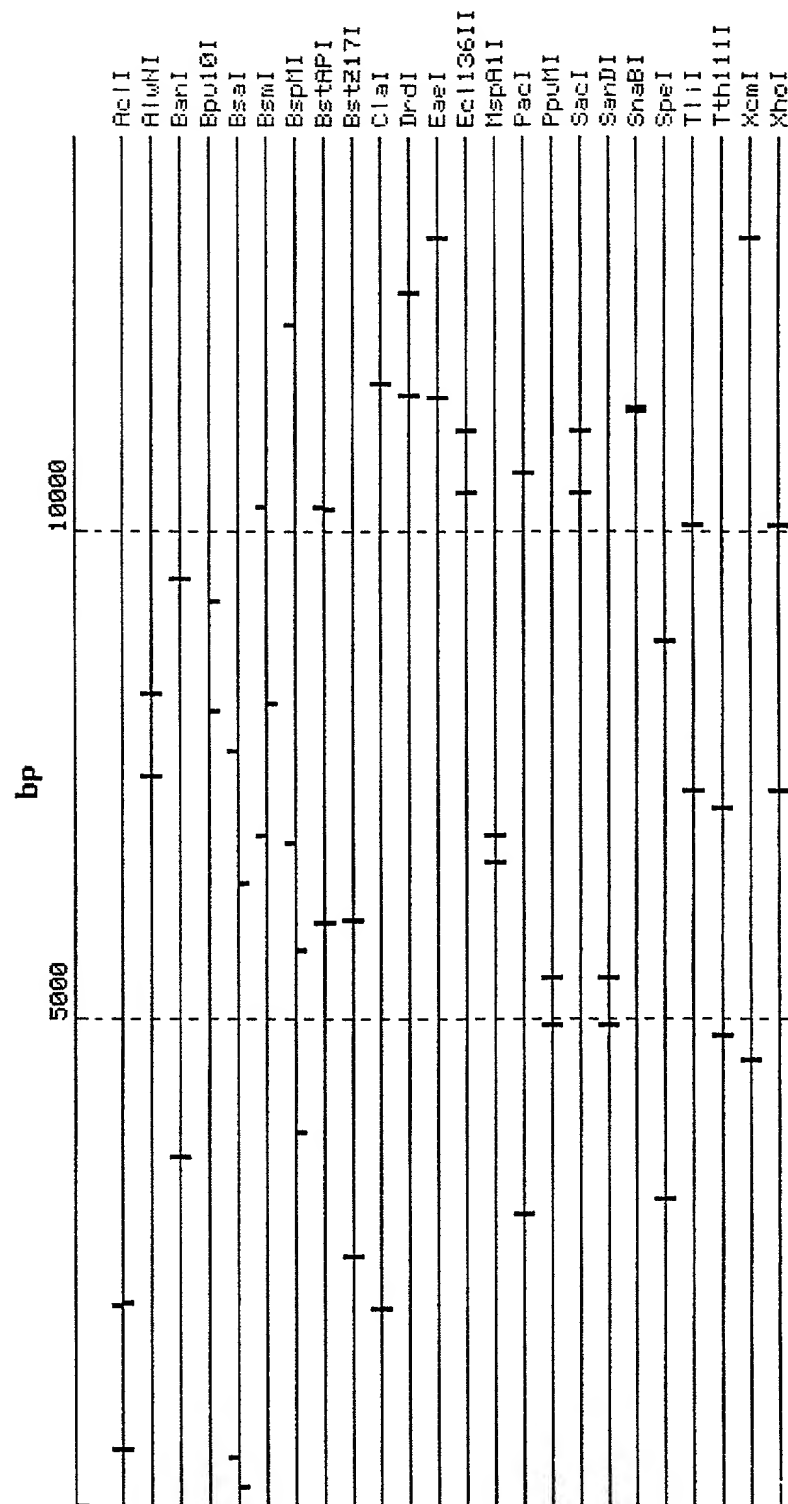


FIGURE 5

[illegible]

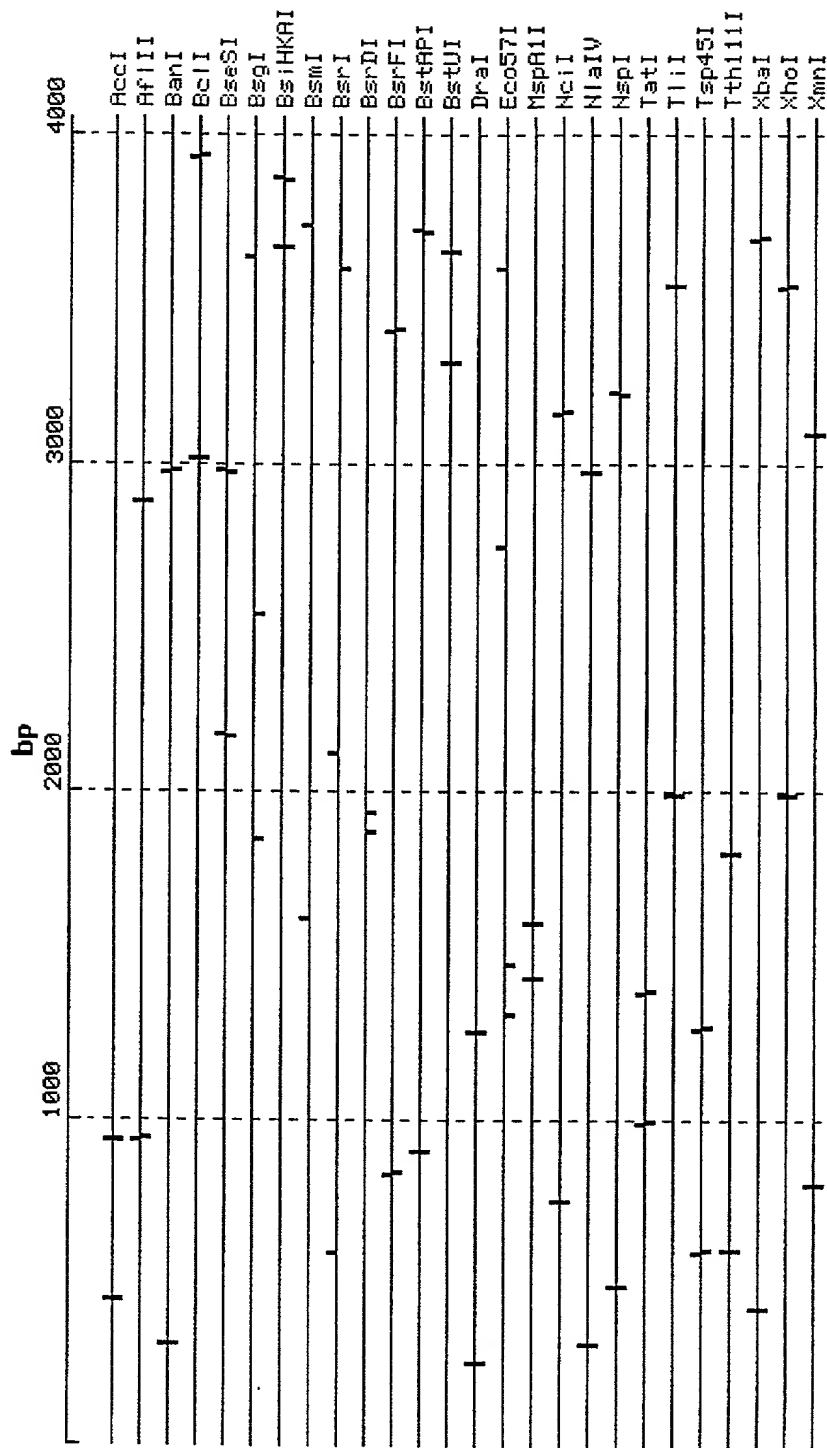


FIGURE 7

6

Sequence Listing



SEQUENCE LISTING

<110> Spalding, Edgar P.
Noh, Bosl

<120> MDR-Like ABC Transporter Gene From
Plants

<130> 13238-00061

<140> herewith
<141> not yet assigned

<150> PCT/US99/22363
<151> 1999-09-24

<150> US 60/101,814
<151> 1998-09-25

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4051

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (94) .. (0)

<223> Translation start codon

<221> misc_feature

<222> (3932) .. (0)

<223> Stop codon

<400> 1

cttgaactc acaaaacaat tgtcagattt tcaagaaaaa cttataaaa caaaaaacat
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tcgttcttc ttactttct taaactcggat ctacaaaaa ccatgtcggg aactaacaca
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aatgatttg gtaaaaaa aatgattta catcaatgg ttcattgaat ccttagatat
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gatatataa aagaagttgg gtctcttgat actgactga gaaactggtg catgtcttc
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tatacactca ccggaattac ttcaaaagac cgtgaatct atgctaagc cgttgtatc
gccgaagcag caatgcaca agtcgaact gttatctt atgttgagga gagttaaggca
cctaagcgt attcggatgc gattcagtat acccttaagc tcggtataa agcggggtg
gctaaagggt tgggttagg atgtacttat ggaatagctt gtatgtcatg ggcattgtg
tttgglatg ctggaagttt tattcggaat ggaacaaccg atggaggaag ggcgtttact

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<110> Spalding, Edgar P.
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<140> herewith

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<221> misc_feature

<222> (3932)...(0)

<223> Stop codon

<400> 1

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tcgtttcttc	ttactttctt	taactcggat	ctacaaaaaa	ccatgtcggg	aactaacaca	180
accgatgcc	agactgttcc	agcagaagca	gagaagaaga	aagaacagag	tttaccattc	240
tttaaaactc	tttcttttgc	tgataaaatt	gattatctct	taatgttcgt	tggttctctt	300
ggtgccattg	ttcatggctc	ttccatgcct	gtcttctttt	tactctttgg	tcaaattggt	360
aatggatttg	gtaaaaacca	aatggattta	catcaaattg	ttcatgaagt	ctctagatat	420
tctctatatt	tcgtctactt	gggttttggt	gtttgcttct	cttcttacgc	agagatagca	480
tgttggatgt	attctggaga	aagacaagta	gcagcattaa	ggaagaaata	tcttgaagca	540
gtattaaaac	aagacgttgg	gttctttgat	actgatgcta	gaactggtga	cattgtcttt	600
agtgtttcta	ctgatactct	tcttgttcaa	gatgccatta	gtgaaaagg	tggaaacttt	660
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tatacactca	cgggaattac	ttcaaagagc	cgtgaatctt	atgctaacgc	cgggtgttat	840
gccgagcagg	caattgctca	agttcgaact	gtttattctt	atgttggaga	gagtaaggca	900
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gctatatctct	ctgctattgt	tgggtgaatg	agtttggggc	aatctttctc	gaatcttggg	1140
gcgttttagta	aaggtaaagc	ggctgggtat	aagttgatgg	agataattaa	ccagagaccg	1200
acgataattc	aagaccggtt	ggatggaaaa	tgtttggatc	aagttcatgg	gaacattgag	1260
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Ala	Asp	Lys	Phe	Asp	Tyr	Leu	Leu	Met	Phe	Val	Gly	Ser	Leu	Gly	Ala
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Ile	Val	His	Gly	Ser	Ser	Met	Pro	Val	Phe	Phe	Leu	Leu	Phe	Gly	Gln
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Met	Val	Asn	Gly	Phe	Gly	Lys	Asn	Gln	Met	Asp	Leu	His	Gln	Met	Val
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His	Glu	Val	Ser	Arg	Tyr	Ser	Leu	Tyr	Phe	Val	Tyr	Leu	Gly	Leu	Val
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Leu	Thr	Gly	Ile	Thr	Ser	Lys	Ser	Arg	Glu	Ser	Tyr	Ala	Asn	Ala	Gly
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Val	Ile	Ala	Glu	Gln	Ala	Ile	Ala	Gln	Val	Arg	Thr	Val	Tyr	Ser	Tyr
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Asp	Val	Thr	Phe	Ser	Tyr	Pro	Ser	Arg	Pro	Asp	Val	Met	Ile	Phe	Arg
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Asn	Phe	Asn	Ile	Phe	Phe	Pro	Ser	Gly	Lys	Thr	Val	Ala	Val	Val	Gly
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Gly	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Val	Ser	Leu	Ile	Glu	Arg	Phe
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Tyr	Asp	Pro	Asn	Ser	Gly	Gln	Ile	Leu	Leu	Asp	Gly	Val	Glu	Ile	Lys
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Asp Phe Ser Asn Pro Ser Thr Arg Arg Thr Arg Ser Thr Arg Leu Ser				
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His Ser Leu Ser Thr Lys Ser Leu Ser Leu Arg Ser Gly Ser Leu Arg				
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His Ala Lys Thr Ser Met Ile Ala Gly Glu Gly Val Ser Asn Ile Arg				
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His Glu Leu Arg Val Pro Gln Lys Arg Ser Leu Ser Leu Tyr Arg Ser				
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Arg	Asn	Ala	Asp	Val	Ile	Ala	Gly	Phe	Asp	Asp	Gly	Val	Ile	Val	Glu							
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Lys	Gly	Asn	His	Asp	Glu	Leu	Met	Lys	Glu	Lys	Gly	Ile	Tyr	Phe	Lys							
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Leu	Val	Thr	Met	Gln	Thr	Ala	Gly	Asn	Glu	Val	Glu	Leu	Glu	Asn	Ala							
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Asp	Ser	Arg	Ser	Ser	Leu	Ile	Arg	Lys	Arg	Ser	Thr	Arg	Arg	Ser	Val							
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Asp	Glu	Ser	Ile	Pro	Pro	Val	Ser	Phe	Trp	Arg	Ile	Met	Lys	Leu	Asn							
				690					695								700					
Leu	Thr	Glu	Trp	Pro	Tyr	Phe	Val	Val	Gly	Val	Phe	Cys	Ala	Ile	Ile							
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Asn	Gly	Gly	Leu	Gln	Pro	Ala	Phe	Ala	Ile	Ile	Phe	Ser	Lys	Ile	Ile							
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Gly	Val	Phe	Thr	Arg	Ile	Asp	Asp	Pro	Glu	Thr	Lys	Arg	Gln	Asn	Ser							
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Asn	Leu	Phe	Ser	Leu	Leu	Phe	Leu	Ala	Leu	Gly	Ile	Ile	Ser	Phe	Ile							
				755					760								765					
Thr	Phe	Phe	Leu	Gln	Gly	Phe	Thr	Phe	Gly	Lys	Ala	Gly	Glu	Ile	Leu							
				770					775								780					
Thr	Lys	Arg	Leu	Arg	Tyr	Met	Val	Phe	Arg	Ser	Met	Leu	Arg	Gln	Asp							
785					790					795								800				
Val	Ser	Trp	Phe	Asp	Pro	Lys	Asn	Thr	Thr	Gly	Ala	Leu	Thr	Thr								
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Arg	Leu	Ala	Asn	Asp	Ala	Ala	Gln	Val	Lys	Gly	Ala	Ile	Gly	Ser	Arg							
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Leu	Ala	Val	Ile	Thr	Gln	Asn	Ile	Ala	Asn	Leu	Gly	Thr	Gly	Ile	Ile							
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 Val Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val Leu Gln Gly Leu
 1045 1050 1055
 Ser Leu Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val Gly Ser Ser
 1060 1065 1070
 Gly Cys Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg Phe Tyr Asp
 1075 1080 1085
 Pro Leu Ala Gly Lys Val Leu Leu Asp Gly Lys Glu Ile Lys Arg Leu
 1090 1095 1100
 Asn Val Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser Gln Glu Pro
 1105 1110 1115 1120
 Ile Leu Phe Asp Cys Ser Ile Ala Glu Asn Ile Ala Tyr Gly Asp Asn
 1125 1130 1135
 Ser Arg Val Val Ser Gln Glu Glu Ile Val Arg Ala Ala Lys Glu Ala
 1140 1145 1150
 Asn Ile His Ala Phe Ile Glu Ser Leu Pro Asn Lys Tyr Ser Thr Lys
 1155 1160 1165
 Val Gly Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile
 1170 1175 1180
 Ala Ile Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu Leu Leu Asp
 1185 1190 1195 1200
 Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val Val Gln Glu
 1205 1210 1215
 Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val Ile Ala His
 1220 1225 1230
 Arg Leu Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val Phe Gln Asn
 1235 1240 1245
 Gly Arg Val Lys Glu His Gly Thr His Gln Gln Leu Leu Ala Gln Lys
 1250 1255 1260
 Gly Ile Tyr Phe Ser Met Val Ser Val Gln Ala Gly Thr Lys Arg Gln
 1265 1270 1275 1280

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 <212> PRT
 <213> Mus musculus

<300>
 <308> Genbank P06795
 <309> 1998-07-15

<400> 4

Ser Asn Ser Ser Leu Glu Glu Glu Met Ala Ile Tyr Ala Tyr Tyr Tyr
 1 5 10 15

Thr Gly Ile Gly Ala Gly Val Leu Ile Val Ala Tyr Ile Gln Val Ser
 20 25 30
 Leu Trp Cys Leu Ala Ala Gly Arg Gln Ile His Lys Ile Arg Gln Lys
 35 40 45
 Phe Phe His Ala Ile Met Asn Gln Glu Ile Gly Trp Phe Asp Val His
 50 55 60
 Asp Val Gly Glu Leu Asn Thr Arg Leu Thr Asp Asp Val Ser Lys Ile
 65 70 75 80
 Asn Asp Gly Ile Gly Asp Lys Ile Gly Met Phe Phe Gln Ser Ile Thr
 85 90 95
 Thr Phe Leu Ala Gly Phe Ile Ile Gly Phe Ile Ser Gly Trp Lys Leu
 100 105 110
 Thr Leu Val Ile Leu Ala Val Ser Pro Leu Ile Gly Leu Ser Ser Ala
 115 120 125
 Leu Trp Ala Lys Val Leu Thr Ser Phe Thr Asn Lys Glu Leu Gln Ala
 130 135 140
 Tyr Ala Lys Ala Gly Ala Val Ala Glu Glu Val Leu Ala Ala Ile Arg
 145 150 155 160
 Thr Val Ile Ala Phe Gly Gly Gln Gln Lys Glu Leu Glu Arg Tyr Asn
 165 170 175
 Lys Asn Leu Glu Glu Ala Lys Asn Val Gly Ile Lys Lys Ala Ile Thr
 180 185 190
 Ala Ser Ile Ser Ile Gly Ile Ala Tyr Leu Leu Val Tyr Ala Ser Tyr
 195 200 205
 Ala Leu Ala Phe Trp Tyr Gly Thr Ser Leu Val Leu Ser Asn Glu Tyr
 210 215 220
 Ser Ile Gly Glu Val Leu Thr Val Phe Phe Ser Ile Leu Leu Gly Thr
 225 230 235 240
 Phe Ser Ile Gly His Leu Ala Pro Asn Ile Glu Ala Phe Ala Asn Ala
 245 250 255
 Arg Gly Ala Ala Phe Glu Ile Phe Lys Ile Ile Asp Asn Glu Pro Ser
 260 265 270
 Ile Asp Ser Phe Ser Thr Lys Gly Tyr Lys Pro Asp Ser Ile Met Gly
 275 280 285
 Asn Leu Glu Phe Lys Asn Val His Phe Asn Tyr Pro Ser Arg Ser Glu
 290 295 300
 Val Gln Ile Leu Lys Gly Leu Asn Leu Lys Val Lys Ser Gly Gln Thr
 305 310 315 320
 Val Ala Leu Val Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val Gln
 325 330 335
 Leu Met Gln Arg Leu Tyr Asp Pro Leu Glu Gly Val Val Ser Ile Asp
 340 345 350
 Gly Gln Asp Ile Arg Thr Ile Asn Val Arg Tyr Leu Arg Glu Ile Ile
 355 360 365
 Gly Val Val Ser Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala Glu
 370 375 380
 Asn Ile Arg Tyr Gly Arg Glu Asp Val Thr Met Asp Glu Ile Glu Lys
 385 390 395 400
 Ala Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro His
 405 410 415
 Gln Phe Asp Thr Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly Gly
 420 425 430
 Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro Lys
 435 440 445
 Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu
 450 455 460
 Ala Val Val Gln Ala Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Thr

465					470					475					480
Ile	Val	Ile	Ala	His	Arg	Leu	Ser	Thr	Val	Arg	Asn	Ala	Asp	Val	Ile
				485						490				495	
Ala	Gly	Phe	Asp	Gly	Gly	Val	Ile	Val	Glu	Gln	Gly	Asn	His	Asp	Glu
			500					505					510		
Leu	Met	Arg	Glu	Lys	Gly	Ile	Tyr	Phe	Lys	Leu	Val	Met	Thr	Gln	Thr
		515					520					525			
Arg	Gly	Asn	Glu	Ile	Glu	Pro	Gly	Asn	Asn	Ala	Tyr	Gly	Ser	Gln	Ser
		530				535					540				
Asp	Thr	Asp	Ala	Ser	Glu	Leu	Thr	Ser	Glu	Glu	Ser	Lys	Ser	Pro	Leu
545					550					555					560
Ile	Arg	Arg	Ser	Ile	Tyr	Arg	Ser	Val	His	Arg	Lys	Gln	Asp	Gln	Glu
			565						570					575	
Arg	Arg	Leu	Ser	Met	Lys	Glu	Ala	Val	Asp	Glu	Asp	Val	Pro	Leu	Val
		580						585					590		
Ser	Phe	Trp	Arg	Ile	Leu	Asn	Leu	Asn	Leu	Ser	Glu	Trp	Pro	Tyr	Leu
		595				600						605			
Leu	Val	Gly	Val	Leu	Cys	Ala	Val	Ile	Asn	Gly	Cys	Ile	Gln	Pro	Val
	610					615					620				
Phe	Ala	Ile	Val	Phe	Ser	Arg	Ile	Val	Gly	Val	Phe	Ser	Arg	Asp	Asp
625					630					635					640
Asp	His	Glu	Thr	Lys	Arg	Gln	Asn	Cys	Asn	Leu	Phe	Ser	Leu	Phe	Phe
				645					650					655	
Leu	Val	Met	Gly	Leu	Ile	Ser	Phe	Val	Thr	Tyr	Phe	Phe	Gln	Gly	Phe
		660						665					670		
Thr	Phe	Gly	Lys	Ala	Gly	Glu	Ile	Leu	Thr	Lys	Arg	Val	Arg	Tyr	Met
		675				680						685			
Val	Phe	Lys	Ser	Met	Leu	Arg	Gln	Asp	Ile	Ser	Trp	Phe	Asp	Asp	His
	690				695						700				
Lys	Asn	Ser	Thr	Gly	Ser	Leu	Thr	Thr	Arg	Leu	Ala	Ser	Asp	Ala	Ser
705					710					715					720
Ser	Val	Lys	Gly	Ala	Met	Gly	Ala	Arg	Leu	Ala	Val	Val	Thr	Gln	Asn
			725						730					735	
Val	Ala	Asn	Leu	Gly	Thr	Gly	Val	Ile	Leu	Ser	Leu	Val	Tyr	Gly	Trp
		740						745					750		
Gln	Leu	Thr	Leu	Leu	Leu	Val	Val	Ile	Ile	Pro	Leu	Ile	Val	Leu	Gly
		755				760						765			
Gly	Ile	Ile	Glu	Met	Lys	Leu	Leu	Ser	Gly	Gln	Ala	Leu	Lys	Asp	Lys
	770					775					780				
Lys	Gln	Leu	Glu	Ile	Ser	Gly	Lys	Ile	Ala	Thr	Glu	Ala	Ile	Glu	Asn
785					790					795					800
Phe	Arg	Thr	Ile	Val	Ser	Leu	Thr	Arg	Glu	Gln	Lys	Phe	Glu	Thr	Met
			805						810					815	
Tyr	Ala	Gln	Ser	Leu	Gln	Val	Pro	Tyr	Arg	Asn	Ala	Met	Lys	Lys	Ala
			820					825					830		
His	Val	Phe	Gly	Ile	Thr	Phe	Ser	Phe	Thr	Gln	Ala	Met	Met	Tyr	Phe
		835				840						845			
Ser	Tyr	Ala	Ala	Cys	Phe	Arg	Phe	Gly	Ala	Tyr	Leu	Val	Ala	Gln	Gln
	850					855					860				
Leu	Met	Thr	Phe	Glu	Asn	Val	Met	Leu	Val	Phe	Ser	Ala	Val	Val	Phe
865					870					875					880
Gly	Ala	Met	Ala	Ala	Gly	Asn	Thr	Ser	Ser	Phe	Ala	Pro	Asp	Tyr	Ala
				885					890					895	
Lys	Ala	Lys	Val	Ser	Ala	Ser	His	Ile	Arg	Ile	Ile	Glu	Lys	Thr	
		900						905				910			
Pro	Glu	Ile	Asp	Ser	Tyr	Ser	Thr	Glu	Gly	Leu	Lys	Pro	Thr	Leu	Leu
		915					920					925			

Glu Gly Asn Val Lys Phe Asn Gly Val Gln Phe Asn Tyr Pro Thr Arg
 930 935 940
 Pro Asn Ile Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys Lys Gly
 945 950 955 960
 Gln Thr Leu Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr Val
 965 970 975
 Val Gln Leu Leu Glu Arg Phe Tyr Asp Pro Met Ala Gly Ser Val Phe
 980 985 990
 Leu Asp Gly Lys Glu Ile Lys Gln Leu Asn Val Gln Trp Leu Arg Ala
 995 1000 1005
 His Leu Gly Ile Val Ser Gln Glu Pro Ile Leu Phe Asp Cys Ser Ile
 1010 1015 1020
 Ala Glu Asn Ile Ala Tyr Gly Asp Asn Ser Arg Ala Val Ser His Glu
 1025 1030 1035 1040
 Glu Ile Val Arg Ala Ala Lys Glu Ala Asn Ile His Gln Phe Ile Asp
 1045 1050 1055
 Ser Leu Pro Asp Lys Tyr Asn Thr Arg Val Gly Asp Lys Gly Thr Gln
 1060 1065 1070
 Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val
 1075 1080 1085
 Arg Gln Pro His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp
 1090 1095 1100
 Thr Glu Ser Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala Arg Glu
 1105 1110 1115 1120
 Gly Arg Thr Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile Gln Asn
 1125 1130 1135
 Ala Asp Leu Ile Val Val Ile Glu Asn Gly Lys Val Lys Glu His Gly
 1140 1145 1150
 Thr His Gln Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met Val
 1155 1160 1165
 Gln Ala Gly Ala Lys Arg Ser
 1170 1175

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 <213> Homo sapiens

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 <309> 1998-07-15

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Trp Lys Leu Thr Leu Val Ile Met Ala Ile Ser Pro Ile Leu Gly Leu
 1 5 10 15
 Ser Ala Ala Val Trp Ala Lys Ile Leu Ser Ala Phe Ser Asp Lys Glu
 20 25 30
 Leu Ala Ala Tyr Ala Lys Ala Gly Ala Val Ala Glu Glu Ala Leu Gly
 35 40 45
 Ala Ile Arg Thr Val Ile Ala Phe Gly Gly Gln Asn Lys Glu Leu Glu
 50 55 60
 Arg Tyr Gln Lys His Leu Glu Asn Ala Lys Glu Ile Gly Ile Lys Lys
 65 70 75 80
 Ala Ile Ser Ala Asn Ile Ser Met Gly Ile Ala Phe Leu Leu Ile Tyr
 85 90 95
 Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Ser Thr Leu Val Ile Ser
 100 105 110

Lys Glu Tyr Thr Ile Gly Asn Ala Met Thr Val Phe Phe Ser Ile Leu
 115 120 125
 Ile Gly Ala Phe Ser Val Gly Gln Ala Ala Pro Cys Ile Asp Ala Phe
 130 135 140
 Ala Asn Ala Arg Gly Ala Ala Tyr Val Ile Phe Asp Ile Ile Asp Asn
 145 150 155 160
 Asn Pro Lys Ile Asp Ser Phe Ser Glu Arg Gly His Lys Pro Asp Ser
 165 170 175
 Ile Lys Gly Asn Leu Glu Phe Asn Asp Val His Phe Ser Tyr Pro Ser
 180 185 190
 Arg Ala Asn Val Lys Ile Leu Lys Gly Leu Asn Leu Lys Val Gln Ser
 195 200 205
 Gly Gln Thr Val Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser Thr
 210 215 220
 Thr Val Gln Leu Ile Gln Arg Leu Tyr Asp Pro Asp Glu Gly Thr Ile
 225 230 235 240
 Asn Ile Asp Gly Gln Asp Ile Arg Asn Phe Asn Val Asn Tyr Leu Arg
 245 250 255
 Glu Ile Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Ser Thr Thr
 260 265 270
 Ile Ala Glu Asn Ile Cys Tyr Gly Arg Gly Asn Val Thr Met Asp Glu
 275 280 285
 Ile Lys Lys Ala Val Lys Glu Ala Asn Ala Tyr Glu Phe Ile Met Lys
 290 295 300
 Leu Pro Gln Lys Phe Asp Thr Leu Val Gly Glu Arg Gly Ala Gln Leu
 305 310 315 320
 Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg
 325 330 335
 Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr
 340 345 350
 Glu Ser Glu Ala Glu Val Gln Ala Ala Leu Asp Lys Ala Arg Glu Gly
 355 360 365
 Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser Thr Val Arg Asn Ala
 370 375 380
 Asp Val Ile Ala Gly Phe Glu Asp Gly Val Ile Val Glu Gln Gly Ser
 385 390 395 400
 His Ser Glu Leu Met Lys Lys Glu Gly Val Tyr Phe Lys Leu Val Asn
 405 410 415
 Met Gln Thr Ser Gly Ser Gln Ile Gln Ser Glu Glu Phe Glu Leu Asn
 420 425 430
 Asp Glu Lys Ala Ala Thr Arg Met Ala Pro Asn Gly Trp Lys Ser Arg
 435 440 445
 Leu Phe Arg His Ser Thr Gln Lys Asn Leu Lys Asn Ser Gln Met Cys
 450 455 460
 Gln Lys Ser Leu Asp Val Glu Thr Asp Gly Leu Glu Ala Asn Val Pro
 465 470 475 480
 Pro Val Ser Phe Leu Lys Val Leu Lys Leu Asn Lys Thr Glu Trp Pro
 485 490 495
 Tyr Phe Val Val Gly Thr Val Cys Ala Ile Ala Asn Gly Gly Leu Gln
 500 505 510
 Pro Ala Phe Ser Val Ile Phe Ser Glu Ile Ile Ala Ile Phe Gly Pro
 515 520 525
 Gly Asp Asp Ala Val Lys Gln Gln Lys Cys Asn Ile Phe Ser Leu Ile
 530 535 540
 Phe Leu Phe Leu Gly Ile Ile Ser Phe Phe Thr Phe Phe Leu Gln Gly
 545 550 555 560
 Phe Thr Phe Gly Lys Ala Gly Glu Ile Leu Thr Arg Arg Leu Arg Ser

Asn Ala Asp Leu Ile Val Val Phe Gln Asn Gly Arg Val Lys Glu His
 1025 1030 1035 1040
 Gly Thr His Gln Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser Met
 1045 1050 1055
 Val Ser Val Gln Ala Gly Thr Gln Asn Leu
 1060 1065

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 <212> PRT
 <213> Mus musculus

<300>
 <308> Genbank P21440
 <309> 1997-11-01

<400> 6

Trp Lys Leu Thr Leu Val Ile Met Ala Ile Ser Pro Ile Leu Gly Leu
 1 5 10 15
 Ser Thr Ala Val Trp Ala Lys Ile Leu Ser Thr Phe Ser Asp Lys Glu
 20 25 30
 Leu Ala Ala Tyr Ala Lys Ala Gly Ala Val Ala Glu Glu Ala Pro Gly
 35 40 45
 Ala Ile Arg Thr Val Ile Ala Phe Gly Gly Gln Asn Lys Glu Leu Glu
 50 55 60
 Arg Tyr Gln Lys His Leu Glu Asn Ala Lys Lys Ile Gly Ile Lys Lys
 65 70 75 80
 Ala Ile Ser Ala Asn Ile Ser Met Gly Ile Ala Phe Leu Leu Ile Tyr
 85 90 95
 Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Ser Thr Leu Val Ile Ser
 100 105 110
 Lys Glu Tyr Thr Ile Gly Asn Ala Met Thr Val Phe Phe Ser Ile Leu
 115 120 125
 Ile Gly Ala Phe Ser Val Gly Gln Ala Ala Pro Cys Ile Asp Ala Phe
 130 135 140
 Ala Asn Ala Arg Gly Ala Ala Tyr Val Ile Phe Asp Ile Ile Asp Asn
 145 150 155 160
 Asn Pro Lys Ile Asp Ser Phe Ser Glu Arg Gly His Lys Pro Asp Asn
 165 170 175
 Ile Lys Gly Asn Leu Glu Phe Ser Asp Val His Phe Ser Tyr Pro Ser
 180 185 190
 Arg Ala Asn Ile Lys Ile Leu Lys Gly Leu Asn Leu Lys Val Lys Ser
 195 200 205
 Gly Gln Thr Val Ala Leu Val Gly Asn Ser Gly Cys Gly Lys Ser Thr
 210 215 220
 Thr Val Gln Leu Leu Gln Arg Leu Tyr Asp Pro Thr Glu Gly Lys Ile
 225 230 235 240
 Ser Ile Asp Gly Gln Asp Ile Arg Asn Phe Asn Val Arg Cys Leu Arg
 245 250 255
 Glu Ile Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Ser Thr Thr
 260 265 270
 Ile Ala Glu Asn Ile Arg Tyr Gly Arg Gly Asn Val Thr Met Asp Glu
 275 280 285
 Ile Glu Lys Ala Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile Met Lys
 290 295 300
 Leu Pro Gln Lys Phe Asp Thr Leu Val Gly Asp Arg Gly Ala Gln Leu
 305 310 315 320

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Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg
 325 330 335
 Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr
 340 345 350
 Glu Ser Glu Ala Glu Val Gln Ala Ala Leu Asp Lys Ala Arg Glu Gly
 355 360 365
 Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser Thr Ile Arg Asn Ala
 370 375 380
 Asp Val Ile Ala Gly Phe Glu Asp Gly Val Ile Val Glu Gln Gly Ser
 385 390 395 400
 His Ser Glu Leu Met Lys Lys Glu Gly Ile Tyr Phe Arg Leu Val Asn
 405 410 415
 Met Gln Thr Ala Gly Ser Gln Ile Leu Ser Glu Glu Phe Glu Ala Arg
 420 425 430
 Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser
 435 440 445
 Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln Val Ala Leu Asp Lys
 450 455 460
 Ala Arg Lys Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser Thr
 465 470 475 480
 Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val Ile Val
 485 490 495
 Glu Lys Gly Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile Tyr Phe
 500 505 510
 Lys Leu Val Thr Met Gln Thr Ala Gly Asn Glu Val Glu Leu Glu Asn
 515 520 525
 Ala Ala Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Leu Leu Asp
 530 535 540
 Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Ala Val Val Gln Ala
 545 550 555 560
 Ala Leu Asp Lys Ala Arg Glu Gly Arg Thr Thr Ile Val Ile Ala His
 565 570 575
 Arg Leu Ser Thr Val Arg Asn Ala Asp Val Ile Ala Gly Phe Asp Gly
 580 585 590
 Gly Val Ile Val Glu Gln Gly Asn His Asp Glu Leu Met Arg Glu Lys
 595 600 605
 Gly Ile Tyr Phe Lys Leu Val Met Thr Gln Thr Arg Gly Asn Glu Ile
 610 615 620
 Glu Pro Gly Asn Asn Ala Val Glu Leu Ser Asp Glu Lys Ala Ala Gly
 625 630 635 640
 Asp Val Ala Pro Asn Gly Trp Lys Ala Arg Ile Phe Arg Asn Ser Thr
 645 650 655
 Lys Lys Ser Leu Lys Ser Pro His Gln Asn Arg Leu Asp Glu Glu Thr
 660 665 670
 Asn Glu Leu Asp Ala Asn Val Pro Pro Val Ser Phe Leu Lys Val Leu
 675 680 685
 Lys Leu Asn Lys Thr Glu Trp Pro Tyr Phe Val Val Gly Thr Val Cys
 690 695 700
 Ala Ile Ala Asn Gly Ala Leu Gln Pro Ala Phe Ser Ile Ile Leu Ser
 705 710 715 720
 Glu Met Ile Ala Ile Phe Gly Pro Gly Asp Asp Ala Val Lys Gln Gln
 725 730 735
 Lys Cys Asn Met Phe Ser Leu Val Phe Leu Gly Leu Gly Val Leu Ser
 740 745 750
 Phe Phe Thr Phe Phe Leu Gln Gly Phe Thr Phe Gly Lys Ala Gly Glu
 755 760 765
 Ile Leu Thr Thr Arg Leu Arg Ser Met Ala Phe Lys Ala Met Leu Arg

770						775						780			
Gln	Asp	Met	Ser	Trp	Phe	Asp	Asp	His	Lys	Asn	Ser	Thr	Gly	Ala	Leu
785					790					795					800
Ser	Thr	Arg	Leu	Ala	Thr	Asp	Ala	Ala	Gln	Val	Gln	Gly	Ala	Thr	Gly
				805					810					815	
Thr	Lys	Leu	Ala	Leu	Ile	Ala	Gln	Asn	Thr	Ala	Asn	Leu	Gly	Thr	Gly
			820					825					830		
Ile	Ile	Ile	Ser	Phe	Ile	Tyr	Gly	Trp	Gln	Leu	Thr	Leu	Leu	Leu	Leu
		835					840					845			
Ser	Val	Val	Pro	Phe	Ile	Ala	Val	Ala	Gly	Ile	Val	Glu	Met	Lys	Met
	850					855					860				
Leu	Ala	Gly	Asn	Ala	Lys	Arg	Asp	Lys	Lys	Glu	Met	Glu	Ala	Ala	Gly
865					870					875					880
Lys	Ile	Ala	Thr	Glu	Ala	Ile	Glu	Asn	Ile	Arg	Thr	Val	Val	Ser	Leu
			885						890					895	
Thr	Gln	Glu	Arg	Lys	Phe	Glu	Ser	Met	Tyr	Val	Glu	Lys	Leu	His	Gly
		900						905					910		
Pro	Tyr	Arg	Asn	Ser	Val	Arg	Lys	Ala	His	Ile	Tyr	Gly	Ile	Thr	Phe
	915						920					925			
Ser	Ile	Ser	Gln	Ala	Phe	Met	Tyr	Phe	Ser	Tyr	Ala	Gly	Cys	Phe	Arg
	930					935					940				
Phe	Gly	Ser	Tyr	Leu	Ile	Val	Asn	Gly	His	Met	Arg	Phe	Lys	Asp	Val
945				950						955					960
Ile	Leu	Val	Phe	Ser	Ala	Ile	Val	Leu	Gly	Ala	Val	Ala	Leu	Gly	His
			965						970					975	
Ala	Ser	Ser	Phe	Ala	Pro	Asp	Tyr	Ala	Lys	Ala	Lys	Leu	Ser	Ala	Ala
		980					985						990		
Tyr	Leu	Phe	Ser	Leu	Phe	Glu	Arg	Gln	Pro	Leu	Ile	Asp	Ser	Tyr	Ser
	995						1000					1005			
Gly	Glu	Gly	Leu	Trp	Pro	Asp	Lys	Phe	Glu	Gly	Ser	Val	Thr	Phe	Asn
	1010					1015					1020				
Glu	Val	Val	Phe	Asn	Tyr	Pro	Thr	Arg	Ala	Asn	Val	Pro	Val	Leu	Gln
1025					1030					1035					1040
Gly	Leu	Ser	Leu	Glu	Val	Lys	Lys	Gly	Gln	Thr	Leu	Ala	Leu	Val	Gly
			1045						1050					1055	
Ser	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Val	Val	Gln	Leu	Leu	Glu	Arg	Phe
		1060						1065					1070		
Tyr	Asp	Pro	Met	Ala	Gly	Ser	Val	Leu	Leu	Asp	Gly	Gln	Glu	Ala	Lys
	1075						1080					1085			
Lys	Leu	Asn	Val	Gln	Trp	Leu	Arg	Ala	Gln	Leu	Gly	Ile	Val	Ser	Gln
	1090					1095					1100				
Glu	Pro	Ile	Leu	Phe	Asp	Cys	Ser	Ile	Ala	Glu	Asn	Ile	Ala	Tyr	Gly
1105				1110						1115					1120
Asp	Asn	Ser	Arg	Val	Val	Pro	His	Asp	Glu	Ile	Val	Arg	Ala	Ala	Lys
			1125						1130					1135	
Glu	Ala	Asn	Ile	His	Pro	Phe	Ile	Glu	Thr	Leu	Pro	Gln	Lys	Tyr	Asn
		1140						1145					1150		
Thr	Arg	Val	Gly	Asp	Lys	Gly	Thr	Gln	Leu	Ser	Gly	Gly	Gln	Lys	Gln
	1155						1160					1165			
Arg	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Ile	Arg	Gln	Pro	Arg	Val	Leu	Leu
	1170					1175					1180				
Leu	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Thr	Glu	Ser	Glu	Lys	Val	Val
1185				1190						1195					1200
Gln	Glu	Ala	Leu	Asp	Lys	Ala	Arg	Glu	Gly	Arg	Thr	Cys	Ile	Val	Ile
			1205						1210					1215	
Ala	His	Arg	Leu	Ser	Thr	Ile	Gln	Asn	Ala	Asp	Leu	Ile	Val	Val	Ile
		1220						1225					1230		

Glu Asn Gly Lys Val Lys Glu His Gly Thr His Gln Gln Leu Leu Ala
 1235 1240 1245
 Gln Lys Gly Ile Tyr Phe Ser Met Val Asn Ile Gln Ala Gly Thr Gln
 1250 1255 1260
 Asn Leu
 1265

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 <212> PRT
 <213> Arabidopsis thaliana

<300>
 <308> Genbank A42150
 <309> 1997-03-13

<400> 7

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Val	Gly	Ala	Ala	Ile	Trp	Ala	Ser	Ser	Trp	Ala	Glu	Ile	Ser	Cys	Trp
			20					25					30		
Met	Trp	Ser	Gly	Glu	Arg	Gln	Thr	Thr	Lys	Met	Arg	Ile	Lys	Tyr	Leu
			35				40					45			
Glu	Ala	Ala	Leu	Asn	Gln	Asp	Ile	Gln	Phe	Phe	Asp	Thr	Glu	Val	Arg
	50					55					60				
Thr	Ser	Asp	Val	Val	Phe	Ala	Ile	Asn	Thr	Asp	Ala	Val	Met	Val	Gln
65					70					75					80
Asp	Ala	Ile	Ser	Glu	Lys	Leu	Gly	Asn	Phe	Ile	His	Tyr	Met	Ala	Thr
				85					90					95	
Phe	Val	Ser	Gly	Phe	Ile	Val	Gly	Phe	Thr	Ala	Val	Trp	Gln	Leu	Ala
			100					105					110		
Leu	Val	Thr	Leu	Ala	Val	Val	Pro	Leu	Ile	Ala	Val	Ile	Gly	Gly	Ile
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His	Thr	Thr	Thr	Leu	Ser	Lys	Leu	Ser	Asn	Lys	Ser	Gln	Glu	Ser	Leu
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